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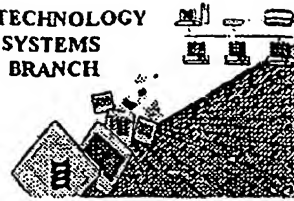
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BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/660,499
Source: FL10
Date Processed by STIC: 2/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>), EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

DATE: 02/24/2004

PATENT APPLICATION: US/10/660,499

TIME: 09:43:29

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02242004\J660499.raw

3 <110> APPLICANT: Seoul National University Industry Foundation
 5 <120> TITLE OF INVENTION: ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
 6 AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
 8 <130> FILE REFERENCE: 20020-02USA
 10 <140> CURRENT APPLICATION NUMBER: US 10/660,499
 11 <141> CURRENT FILING DATE: 2003-09-12
 13 <150> PRIOR APPLICATION NUMBER: KR 2003-19069
 14 <151> PRIOR FILING DATE: 2003-03-27
 16 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: KopatentIn 1.71

ERRORED SEQUENCES

pp 1-4
 Does Not Comply
 Corrected Diskette Needed

225 <210> SEQ ID NO: 9
 226 <211> LENGTH: 29
 227 <212> TYPE: DNA
 228 <213> ORGANISM: Artificial Sequence
 230 <220> FEATURE:
 231 <223> OTHER INFORMATION: Primer
 234 <400> SEQUENCE: 9
 235 agcaagcttg gagttgatgg gaataatca
 E--> 239 1 *delete*

29

see pp 2-3 for more errors

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<400> 1
gcaagagctt caacctctca tcattaggca ttcagcaagc aagaaaaaaa a 51
atg one space only ggc one space only aaa one space only tat one space only atg one space only ctt one space only gtt one space only ttg one space only ggt one space only agc one space only ctc att one space only gga tta one space only tgc tgt 99
Met, Gly, Lys, Ile, Met, Leu, Val, Leu, Gly, Ser, Leu, Ile, Gly, Leu, Cys, Cys
1 one space 5 10 one space 15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
20 25 30

sample of invalid amino acid placement
in sequence 1.

Per 1.822 of Sequence Rules, insert only one space
between codons and amino acids; also, place amino acid
directly under its codon

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<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3 *see p. 4 for error explanation*
nnnggatccga yggatcggg acnattggggyg gygctgygyt angg

44

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4 *see p. 4*
nnngatccctt kswytgccar tnnnscccc arttnck

37

<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 5 *see p. 4*
gaygcwsttg ggnatggg nngggcgtgy ggtayggga ayytntaygc nactgggtay 60
gggacnmgna cngcngcnyr nwsnagggg ythtttaayg ayggngcws ngyggncar 120
tgytayaara thathtgyga ytayaarwsn gaywsnngt ggtgyathaa rggngnwsn 180
gnactgtga cngcnaanaa yttytgycon cnaaytttg cnytncnaa yaayaaygon 240
ggnggtgya ayconcnnyt naarcaytty gayatgggc arcngcngtg ggaraarath 300
ggathtaym ngngngnat hgtncngtn ythttycarm cngtncngtg yaaraarcay 360
ggngngtnm gnttywngt naaygonmng gaytaytttg aryngtntt mathwsnaay 420
gngngngng cngnwsnat ncarwsnngn ttyathaarg nwsnaarac ngngtggatg 480
gnatgwsnm gnaaytggg nwsnaaytgg carwsnaay 519

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004

TIME: 09:43:30

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02242004\J660499.raw

error explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 1,2,14,17,20,23,42

Seq#:4; N Pos. 1,2,23,24,26,35

Seq#:5; N Pos. 6,9,12,15,21,24,27,33,39,45,51,54,57,63,66,69,72,75,78,81,84

Seq#:5; N Pos. 87,90,93,105,108,111,117,150,156,159,174,177,180,183,186,189

Seq#:5; N Pos. 192,195,198,210,213,222,225,228,240,243,255,258,261,279,285

Seq#:5; N Pos. 288,303,312,315,318,324,327,330,333,342,345,348,363,366,369

Seq#:5; N Pos. 372,378,381,387,390,405,408,411,417,423,426,429,432,435,438

Seq#:5; N Pos. 447,450,462,465,471,474,483,489,492,501,504,516

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004

TIME: 09:43:30

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02242004\J660499.raw

L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:139 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
 L:139 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
 L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:152 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
 L:152 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
 L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
 L:165 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
 L:165 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
 L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
 M:341 Repeated in SeqNo=5
 L:239 M:254 E: No. of Bases conflict, this line has no nucleotides.